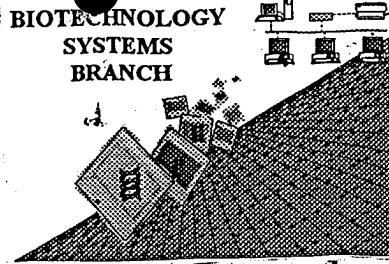12013    1655

# RAW SEQUENCE LISTING
# ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: ___09/345,761A___

Source: ___1600___

Date Processed by STIC: ___11/28/01___

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
 PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
 PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE __CHECKER VERSION 3.0 PROGRAM__, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

## Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

# Raw Sequence Listing Error Summary

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
   Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
   prevent "wrapping."

2_____Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3_____Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
   Numbering   use space characters, instead.

4_____Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
   ensure your subsequent submission is saved in ASCII text.

5_____Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules,
   each n or Xaa can only represent a single residue. Please present the maximum number of each
   residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
   "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
   previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
   the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
   Artificial or Unknown sequences.

7_____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
   (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
   (i)   'SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
   (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
   This sequence is intentionally skipped

   Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
   (NEW RULES)   <210> sequence id number
   <400> sequence id number
   000

9_____Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
   (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
   In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10_____Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
   Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
   is Artificial Sequence

11_____Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
   Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
   "Unknown." Please explain source of genetic material in <220> to <223> section.
   (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12_____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
   "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
   listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

AMC – Biotechnology Systems Branch – 06/04/2001

1600

RAW SEQUENCE LISTING                    DATE: 11/28/2001
PATENT APPLICATION:  US/09/345,761A      TIME: 13:24:17

Input Set : **A:\Q54969 - 09-345,761 Sequence Listing.txt**
Output Set: **N:\CRF3\11212001\I345761A.raw**

*Does Not Comply*
*Corrected Diskette Needed*

```
 3 <110> APPLICANT: ISHIGURO, Takahiko
 4        SAITOH, Juichi
 5        ISHIZUKA, Tetsuya
 7 <120> TITLE OF INVENTION: METHOD OF ASSAY OF TARGET NUCLEIC ACID
 9 <130> FILE REFERENCE: Q54969
11 <140> CURRENT APPLICATION NUMBER: US 09/345,761A
12 <141> CURRENT FILING DATE: 1999-07-01
14 <150> PRIOR APPLICATION NUMBER: JP 10-186434
15 <151> PRIOR FILING DATE: 1998-07-01
17 <160> NUMBER OF SEQ ID NOS: 7
19 <170> SOFTWARE: PatentIn version 3.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 50
23 <212> TYPE: DNA
24 <213> ORGANISM: synthetic construct
26 <400> SEQUENCE: 1
27 atttaggtga cactatagaa tacaacactc caccatagat cactcccctg          50
30 <210> SEQ ID NO: 2
31 <211> LENGTH: 19
32 <212> TYPE: DNA
33 <213> ORGANISM: synthetic construct
35 <400> SEQUENCE: 2
36 actcgcaagc accctatca                                           19
39 <210> SEQ ID NO: 3
40 <211> LENGTH: 11
41 <212> TYPE: DNA
42 <213> ORGANISM: synthetic construct
44 <400> SEQUENCE: 3
45 gtcgccccca a                                                   11
48 <210> SEQ ID NO: 4
49 <211> LENGTH: 133
50 <212> TYPE: RNA
51 <213> ORGANISM: synthetic construct
53 <400> SEQUENCE: 4
54 gggaaagcuu gcaugccugc aggucgacuc uagaggaucc ccggguaccg agcucgaauu   60
56 ccuugggggc gacacuccac cauagaucac uccccuguga ggaacuacug ucuucacgca  120
58 gaaagcgucu agc                                                 133
61 <210> SEQ ID NO: 5
62 <211> LENGTH: 13
63 <212> TYPE: DNA
64 <213> ORGANISM: synthetic construct
66 <400> SEQUENCE: 5
67 ctcgcggggg ctg                                                 13
70 <210> SEQ ID NO: 6
71 <211> LENGTH: 315
72 <212> TYPE: DNA
73 <213> ORGANISM: Synthetic Construct
```

→invalid, see error summary sheet,
Item 10

RAW SEQUENCE LISTING       DATE: 11/28/2001
PATENT APPLICATION:   US/09/345,761A      TIME: 13:24:17

Input Set : **A:\Q54969 - 09-345,761 Sequence Listing.txt**
Output Set: **N:\CRF3\11212001\I345761A.raw**

```
 75 <400> SEQUENCE: 6
 76 atttaggtga cactatagaa tacaacactc caccatagat cactcccctg tgaggaacta      60
 78 ctgtcttcac gcagaaagcg tctagccatg gcgttagtat gagtgtcgtg cagcctccag     120
 80 gaccccccct cccgggagag ccatagtggt ctgcggaacc ggtgagtaca ccggaattgc     180
 82 caggacgacc gggtcctttc ttggatcaac ccgctcaatg cctggagatt tgggcgtgcc     240
 84 cccgcgagac tgctagccga gtagtgttgg gtcgcgaaag gccttgtggt actgcctgat     300
 86 agggtgcttg cgagt                                                       315
 89 <210> SEQ ID NO: 7
 90 <211> LENGTH: 298
 91 <212> TYPE: RNA
 92 <213> ORGANISM: Synthetic Construct
 94 <400> SEQUENCE: 7
 95 gaauacaaca cuccaccaua gaucacuccc cugugaggaa cuacugucuu cacgcagaaa      60
 97 gcgucuagcc auggcguuag uaugaguguc gugcagccuc caggaccccc ccucccggga     120
 99 gagccauagu ggucugcgga accggugagu acaccggaau ugccaggacg accggguccu     180
101 uucuuggauc aacccgcuca augccuggag auuugggcgu gcccccgcga gacugcuagc     240
103 cgaguagugu ugggucgcga aaggccuugu gguacugccu gauaggggugc uugcgagu      298
```

**VERIFICATION SUMMARY**                DATE: 11/28/2001
PATENT APPLICATION:   **US/09/345,761A**     TIME: 13:24:18

Input Set : **A:\Q54969 - 09-345,761 Sequence Listing.txt**
Output Set: **N:\CRF3\11212001\I345761A.raw**